

Fig. 1

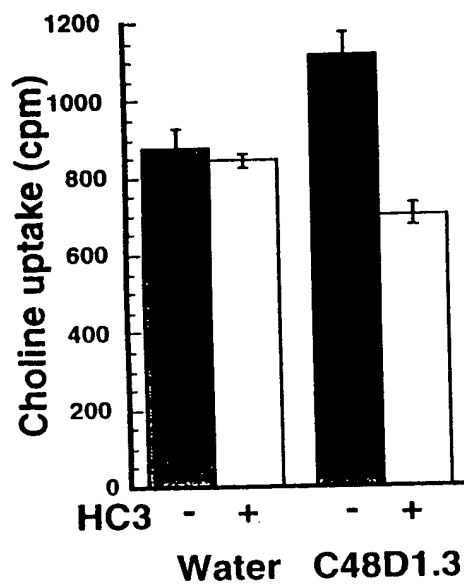


Fig. 2

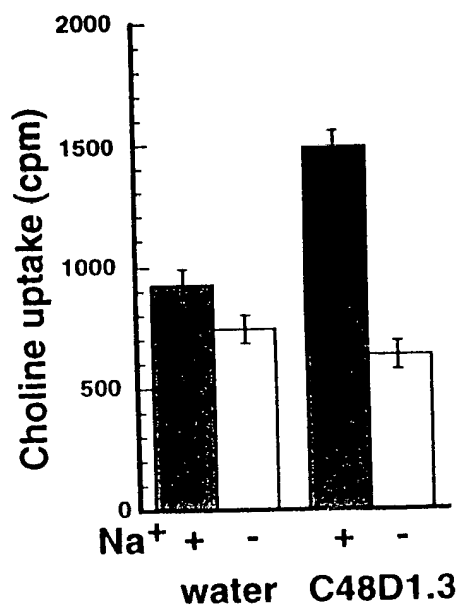


Fig. 3

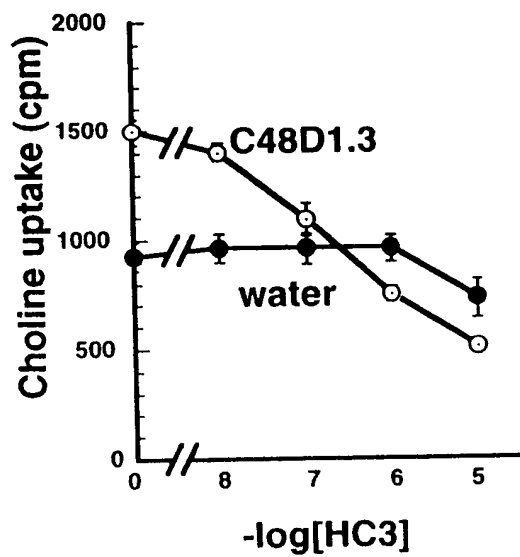


Fig. 4

CHT1	MPFHVEGVVAIDFYLIPLVGIWAANKNS-----GNAEERSEA LYGGRIGLLVGGF	56
cht-1	-MADLGVAIVFYLIPLVGIWAGRKSSKELESAGAAIEEVLAGRNIIGTLVGIF	59
I		
CHT1	TMTATWVGGGYINGTAEAYGPGCGLAWAQAPGYSLSLGGGLFAKPMRS GY TMLD	116
cht-1	TMTATWVGGA YINGTAEALYNGGLLGQAPGYLSLGGGLFAKPMRE GY TMLD	117
II		
CHT1	PFQITYGKRGGLPALMGEMFWAAATISALGATISVI DGDNISVIT SALTALYT	176
cht-1	PFQIKYGRIGGLYPALLGETFWTAATISALGATISVI GGDNASVIT SACTALYT	177
III		
CHT1	VGGLYVAYTDVVQLFCIFGLWISVPFALSHPVVDIGFTAVHAKYQSPWLTIES-V	235
cht-1	TGGYYVAYTDVVQLFCIFGLWCVPAAVHDGAKDTSRNAG-----DWLGETGGFK	231
V		
CHT1	EYVTWLDNLLLVLGGIPWQAYFQRLSSSATYAQVLSFAAFGCCMA PAICIGATG	295
cht-1	ETSLWIDC LLLVLGGIPWQVYFQRLSSKAHGAQTLSEFAGVGCMA PPALIGATA	291
VI		
CHT1	ASTDWNQTA YGFP PKTKKEAD-----MTLPVLQYLCPVYISFGLGAVSAAMSSAD	349
cht-1	RNTDWRMTDYSPWNGTKVESIPDPKRMVWPLVQYLTPIRI FGLGAVSAAMSSAD	351
VII		
CHT1	SSLSSASSMFARNITCLSRQASDKEIWMRIIVFVGASATAMALLTCTYGLWYLS	409
cht-1	SSVLSAASSMFARNITKLRPASEKEVITVMRIALCVGIMATIMALTIDSYGLWYLC	411
VIII		
CHT1	DLVYITFPQLLCVIEKGNITYGAVAGYIFGLFLRITGGEPYLYLP FYPGYYPDK	469
cht-1	DLVYIITFPQLLCVIMPRNTYGSAGYAVGLVLRITGGEPVSLPA HYPMYT-D	469
IX		
CHT1	NGIYNQRFPFRTLSMVTSEFTNICVSYLAKYLFESGTLPPKLDITDAVVS R---HSEENM	526
cht-1	G---VOYFPFRTITAMSSMATIYIVSIQSEKLFSGRLSPENDYMGCVNIPIDHVPLPS	526
X		
CHT1	DKITLVNRNENIKLNELAPVKPRQSTLSSTFTNKEALLDVDSSPEGSGT DNLQ	580
cht-1	DVSTAVSSE--TLNMKAPNGTPAPVHPNQQP SDENTLLHPYSDQSYSTNSN--	576
XII		

Fig. 5

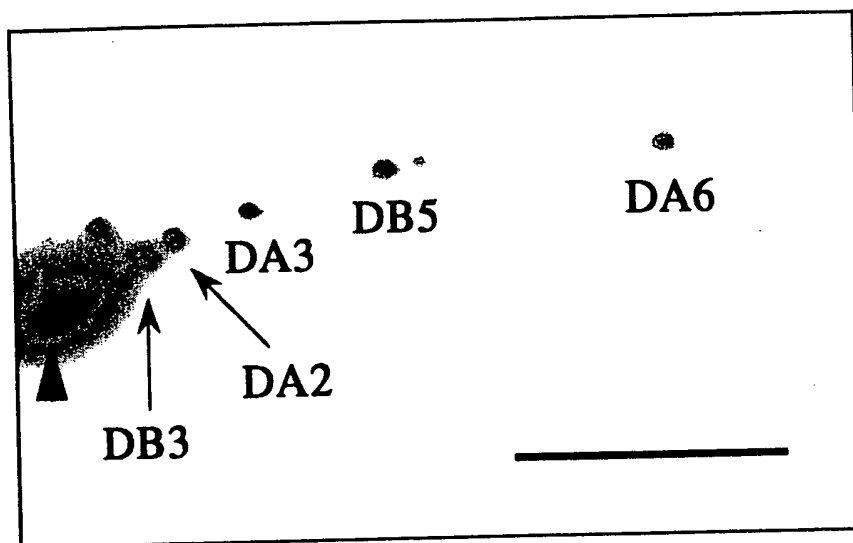


Fig. 6

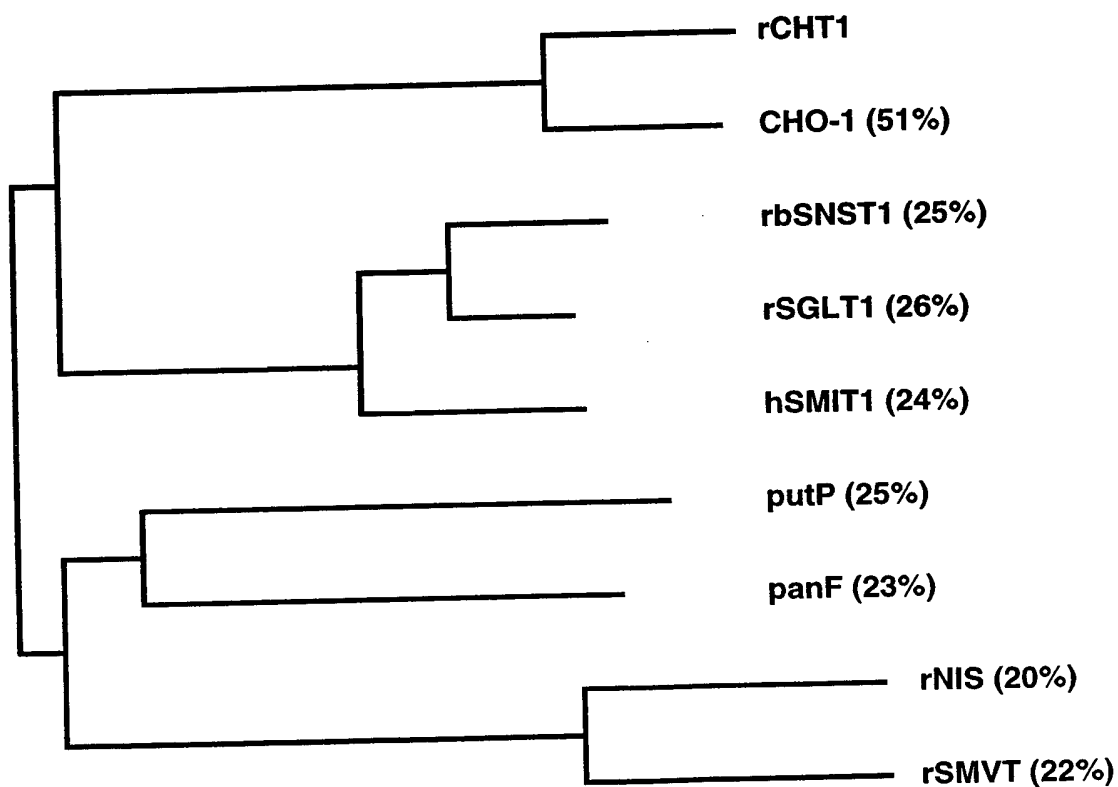


Fig. 7

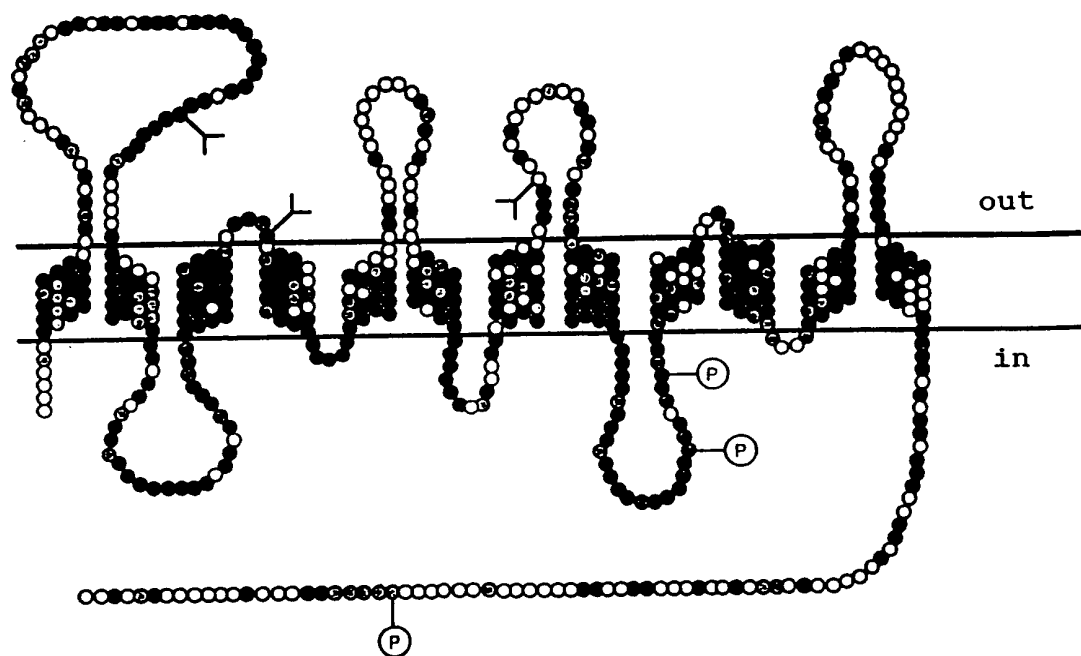


Fig. 8

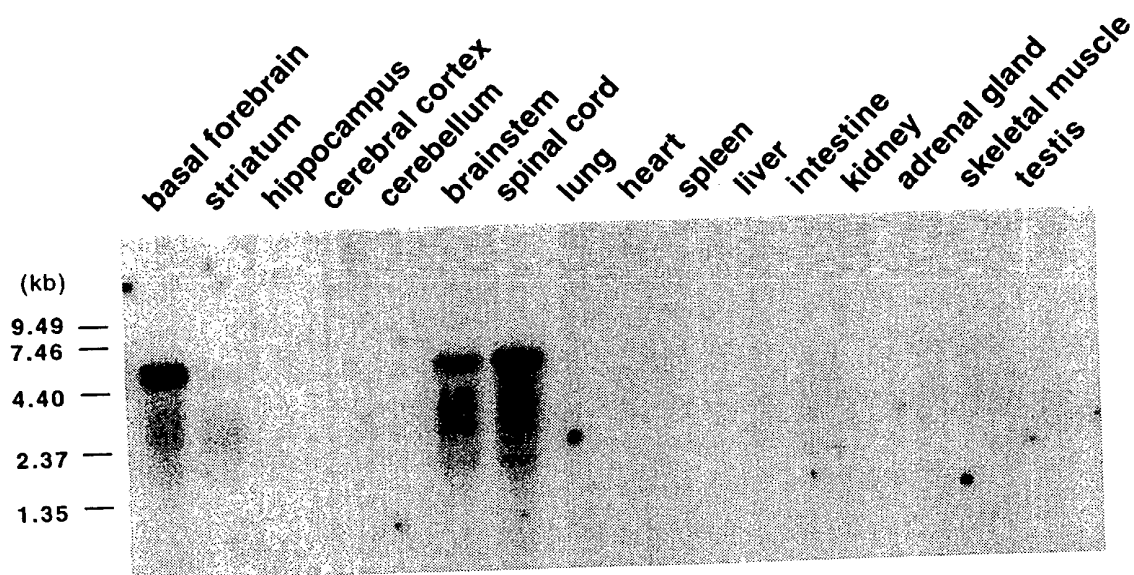


Fig. 9



Fig. 10

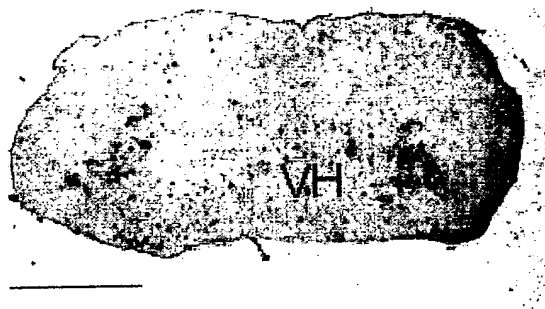


Fig. 11

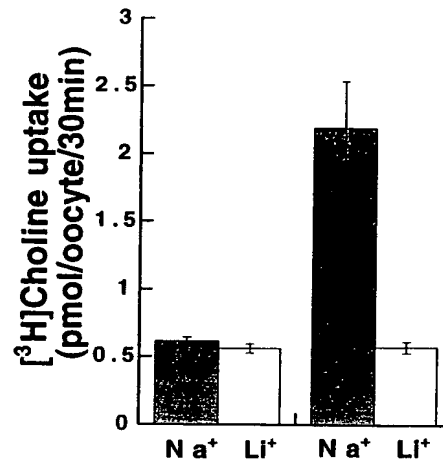


Fig. 12

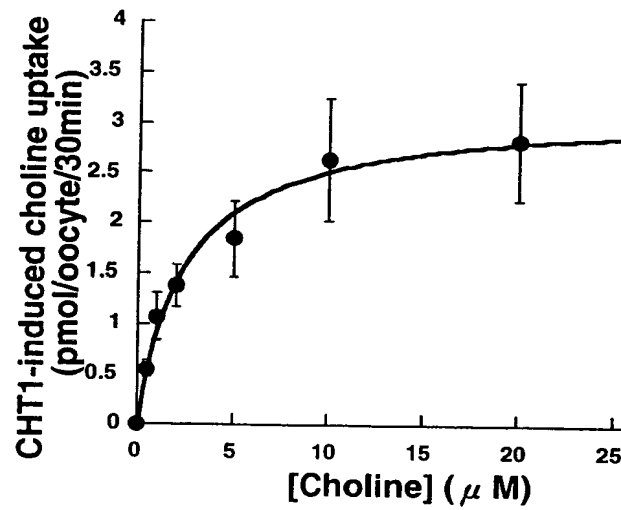


Fig. 13

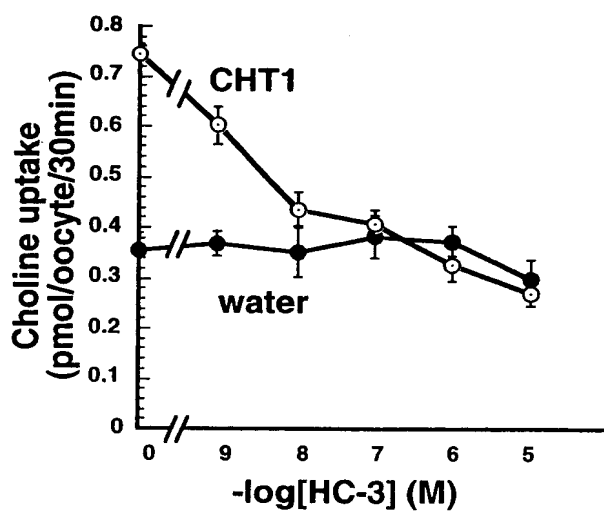


Fig. 14

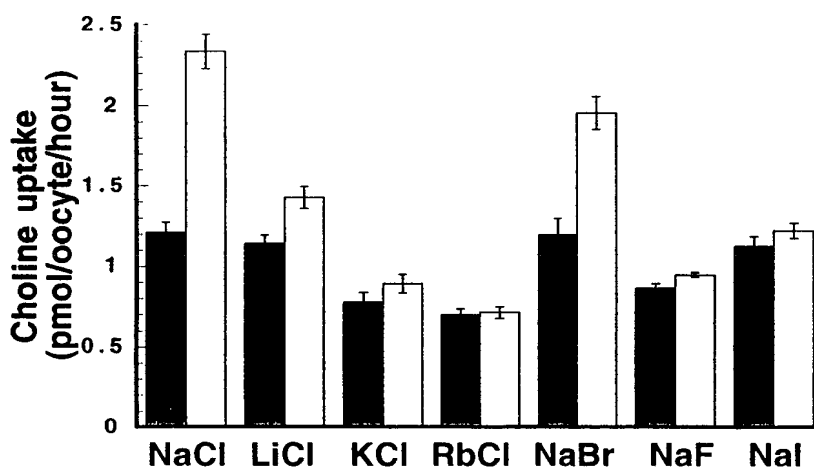


Fig. 15

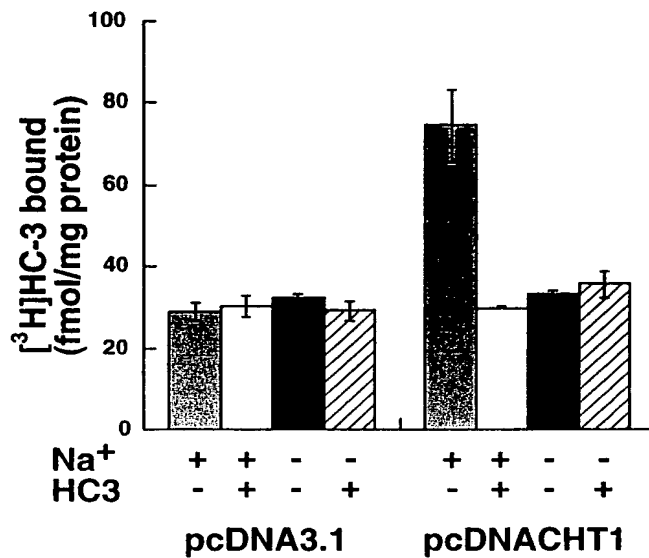


Fig. 16

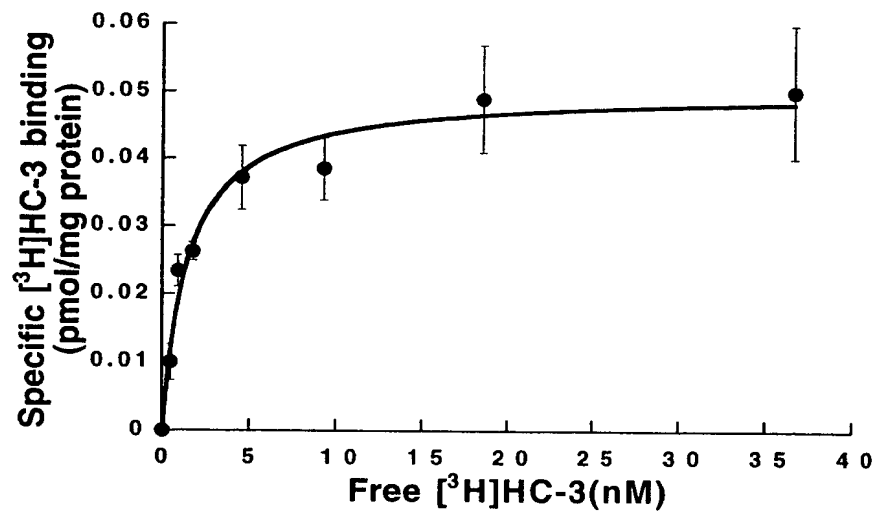


Fig. 17

